

SEQUENCE LISTING

<110> Zhou, Ming-Ming

<120> METHODS OF IDENTIFYING MODULATORS OF THE FGF RECEPTOR

<130> 2459-1-002N

<140> UNKNOWN

<141> 2001-01-11

<150> 60/175,867

<151> 2000-01-12

<160> 7

<170> PatentIn Ver. 2.0

<210> 1

<211> 508

<212> PRT

<213> Homo sapien

<400> 1

Met Gly Ser Cys Cys Ser Cys Pro Asp Lys Asp Thr Val Pro Asp Asn  
1 5 10 15

His Arg Asn Lys Phe Lys Val Ile Asn Val Asp Asp Asp Gly Asn Glu  
20 25 30

Leu Gly Ser Gly Ile Met Glu Leu Thr Asp Thr Glu Leu Ile Leu Tyr  
35 40 45

Thr Arg Lys Arg Asp Ser Val Lys Trp His Tyr Leu Cys Leu Arg Arg  
50 55 60

Tyr Gly Tyr Asp Ser Asn Leu Phe Ser Phe Glu Ser Gly Arg Arg Cys  
65 70 75 80

Gln Thr Gly Gln Gly Ile Phe Ala Phe Lys Cys Ala Arg Ala Glu Glu  
85 90 95

Leu Phe Asn Met Leu Gln Glu Ile Met Gln Asn Asn Ser Ile Asn Val  
100 105 110

Val Glu Glu Pro Val Val Glu Arg Asn Asn His Gln Thr Glu Leu Glu  
115 120 125

Val Pro Arg Thr Pro Arg Thr Pro Thr Thr Pro Gly Phe Ala Ala Gln  
130 135 140

Asn Leu Pro Asn Gly Tyr Pro Arg Tyr Pro Ser Phe Gly Asp Ala Ser  
145 150 155 160

Ser His Pro Ser Ser Arg His Pro Ser Val Gly Ser Ala Arg Leu Pro  
165 170 175

Ser Val Gly Glu Glu Ser Thr His Pro Leu Leu Val Ala Glu Glu Gln  
180 185 190

Val His Thr Tyr Val Asn Thr Thr Gly Val Gln Glu Glu Arg Lys Asn  
195 200 205

Arg Thr Ser Val His Val Pro Leu Glu Ala Arg Val Ser Asn Ala Glu  
210 215 220

Ser Ser Thr Pro Lys Glu Glu Pro Ser Ser Ile Glu Asp Arg Asp Pro  
225 230 235 240

Gln Ile Leu Leu Glu Pro Glu Gly Val Lys Phe Val Leu Gly Pro Thr  
245 250 255

Pro Val Gln Lys Gln Leu Met Glu Lys Glu Lys Leu Glu Gln Leu Gly  
260 265 270

Arg Asp Gln Val Ser Gly Ser Gly Ala Asn Asn Thr Glu Trp Asp Thr  
275 280 285

Gly Tyr Asp Ser Asp Glu Arg Arg Asp Ala Pro Ser Val Asn Lys Leu  
290 295 300

Val Tyr Glu Asn Ile Asn Gly Leu Ser Ile Pro Ser Ala Ser Gly Val  
305 310 315 320

Arg Arg Gly Arg Leu Thr Ser Thr Ser Thr Ser Asp Thr Gln Asn Ile  
325 330 335

Asn Asn Ser Ala Gln Arg Arg Thr Ala Leu Leu Asn Tyr Glu Asn Leu  
340 345 350

Pro Ser Leu Pro Pro Val Trp Glu Ala Arg Lys Leu Ser Arg Asp Glu  
355 360 365

Asp Asp Asn Leu Gly Pro Lys Thr Pro Ser Leu Asn Gly Tyr His Asn  
370 375 380

Asn Leu Asp Pro Met His Asn Tyr Val Asn Thr Glu Asn Val Thr Val  
385 390 395 400

Pro Ala Ser Ala His Lys Ile Glu Tyr Ser Arg Arg Arg Asp Cys Thr  
405 410 415

Pro Thr Val Phe Asn Phe Asp Ile Arg Arg Pro Ser Leu Glu His Arg  
420 425 430

Gln Leu Asn Tyr Ile Gln Val Asp Leu Glu Gly Gly Ser Asp Ser Asp  
435 440 445

Asn Pro Gln Thr Pro Lys Thr Pro Thr Thr Pro Leu Pro Gln Thr Pro  
450 455 460

Thr Arg Arg Thr Glu Leu Tyr Ala Val Ile Asp Ile Glu Arg Thr Ala  
465 470 475 480

Ala Met Ser Asn Leu Gln Lys Ala Leu Pro Arg Asp Asp Gly Thr Ser  
485 490 495

Arg Lys Thr Arg His Asn Ser Thr Asp Leu Pro Met  
500 505

<210> 2  
<211> 822  
<212> PRT  
<213> Mouse

<400> 2  
Met Trp Gly Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala  
1 5 10 15

Thr Leu Cys Thr Ala Arg Pro Ala Pro Thr Leu Pro Glu Gln Ala Gln  
20 25 30

Pro Trp Gly Val Pro Val Glu Val Glu Ser Leu Leu Val His Pro Gly  
35 40 45

Asp Leu Leu Gln Leu Arg Cys Arg Leu Arg Asp Asp Val Gln Ser Ile  
50 55 60

Asn Trp Leu Arg Asp Gly Val Gln Leu Val Glu Ser Asn Arg Thr Arg  
65 70 75 80

Ile Thr Gly Glu Glu Val Glu Val Arg Asp Ser Ile Pro Ala Asp Ser  
85 90 95

Gly Leu Tyr Ala Cys Val Thr Ser Ser Pro Ser Gly Ser Asp Thr Thr  
100 105 110

Tyr Phe Ser Val Asn Val Ser Asp Ala Leu Pro Ser Ser Glu Asp Asp  
115 120 125

Asp Asp Asp Asp Asp Ser Ser Glu Glu Lys Glu Thr Asp Asn Thr  
130 135 140

Lys Pro Asn Arg Arg Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys  
145 150 155 160

Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe  
165 170 175

Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys  
180 185 190

Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val  
195 200 205

Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp  
210 215 220

Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn  
225 230 235 240

His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile  
245 250 255

Leu Gln Ala Gly Leu Pro Ala Asn Glu Thr Val Ala Leu Gly Ser Asn  
260 265 270

Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln  
275 280 285

Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn  
290 295 300

Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp  
305 310 315 320

Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala  
325 330 335

Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His  
340 345 350

Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val  
355 360 365

Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala  
370 375 380

Phe Leu Ile Ser Cys Met Leu Gly Ser Val Ile Ile Tyr Lys Met Lys  
385 390 395 400

Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys  
405 410 415

Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp  
420 425 430

Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg  
435 440 445

Leu Ser Ser Ser Gly Thr Pro Met Pro Ala Gly Val Ser Glu Tyr Glu  
450 455 460

Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu  
465 470 475 480

Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu  
485 490 495

Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala  
500 505 510

Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu  
515 520 525

Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile  
530 535 540

Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile  
545 550 555 560

Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg  
565 570 575

Arg Pro Pro Gly Leu Glu Tyr Cys Tyr Asn Pro Ser His Asn Pro Glu  
580 585 590

Glu Gln Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala  
595 600 605

Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg Asp Leu  
610 615 620

Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala  
625 630 635 640

Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr Lys Lys  
645 650 655

Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu  
660 665 670

Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val  
675 680 685

Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Val  
690 695 700

Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp  
705 710 715 720

Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys  
725 730 735

Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu  
740 745 750

Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Ser Gln Glu Tyr Leu Asp  
755 760 765

Leu Ser Ile Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg  
770 775 780

Ser Ser Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro  
785 790 795 800

Leu Pro Glu Glu Pro Cys Leu Pro Arg His Pro Thr Gln Leu Ala Asn  
805 810 815

Ser Gly Leu Lys Arg Arg  
820

<210> 3  
<211> 22  
<212> PRT  
<213> Mouse

<400> 3  
His Ser Gln Met Ala Val His Lys Leu Ala Lys Ser Ile Pro Leu Arg  
1 5 10 15  
  
Arg Gln Val Thr Val Ser  
20

<210> 4  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
tyrosine-phosphorylated peptide

<220>  
<223> X = phosphotyrosine

<400> 4  
Leu Val Ile Ala Gly Asn Pro Ala Xaa Arg Ser  
1 5 10

<210> 5  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: consensus

<220>  
<223> Xaa can be any amino acid

<400> 5  
Val Xaa Xaa Leu Xaa Xaa Xaa Ile Xaa Leu Xaa Arg Xaa Val Xaa Val  
1 5 10 15

<210> 6  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: motif

<220>

<223> X in the 3rd position= any amino acid

<220>

<223> X in the 4th position= phosphotyrosine

<400> 6

Asn Pro Xaa Xaa

1

<210> 7

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
peptide derived from TrkA receptor

<400> 7

His Ile Ile Glu Asn Pro Gln Xaa Phe Ser Asp Ala

1

5

10